

**Linear Stochastic Modeling for Genetic Regulatory Networks**

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Modelling and determining of genetic regulatory networks from genomic data poses a key scientific challenge with potentially high industrial pay-offs. Recently, a wide variety of methodologies to infer genetic regulatory networks from gene expression data has been proposed in literatures. However, the large number of genes, the limited noisy measurements, and the complex nature of gene regulation make the studying of the genetic regulatory networks from genomic data extremely challenging.

In this paper, we present a learning stochastic and discrete time model with continuous states. This model is based on the principles of discrete time linear stochastic dynamic systems. We employ this linear stochastic regulation model and use the resulting likelihood function of the model for model learning purpose. Overall, we develop a framework for discovering and modelling gene networks by integrating the time-series expression data and the genomic location data in the context of prior biological knowledge. The proposed framework allows us to statistically capture the possible time-varying dependencies among the different components in the regulatory network. The contributions of our work are two folds: First, we propose a linear stochastic model by taking the time-varying and the stochastic characteristics into design account. Second, we increase the inferential capability of the proposed framework by incorporating multiple genomic data sources and prior knowledge from previous studies. We demonstrate our proposed approach on the yeast cell cycle application. The results are consistent with existing studies in the literatures, and also suggest new hypotheses for future investigation.